FIG.1

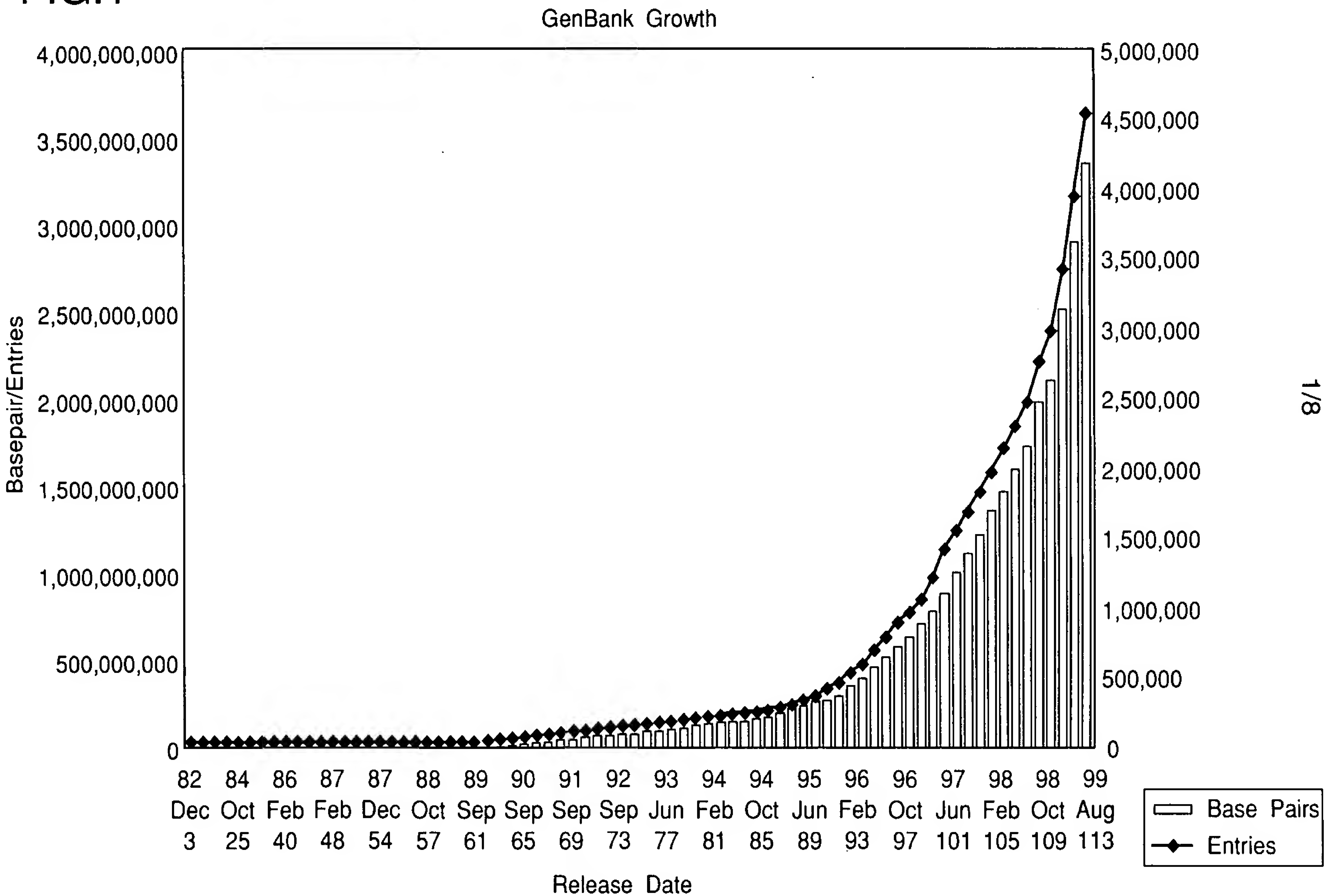

GenBank Growth
Basepair/Entries
4,000,000,000
3,500,000,000
3,000,000,000
2,500,000,000
2,000,000,000
1,500,000,000
1,000,000,000
500,000,000
0
5,000,000
4,500,000
4,000,000
3,500,000
3,000,000
2,500,000
2,000,000
1,500,000
1,000,000
500,000
0
82 Dec 3
84 Oct 25
86 Feb 40
87 Feb 48
87 Dec 54
88 Oct 57
89 Sep 61
90 Sep 65
91 Sep 69
92 Sep 73
93 Jun 77
94 Feb 81
94 Oct 85
95 Jun 89
96 Feb 93
96 Oct 97
97 Jun 101
98 Feb 105
98 Oct 109
99 Aug 113
Release Date
Base Pairs
Entries

FIG.2

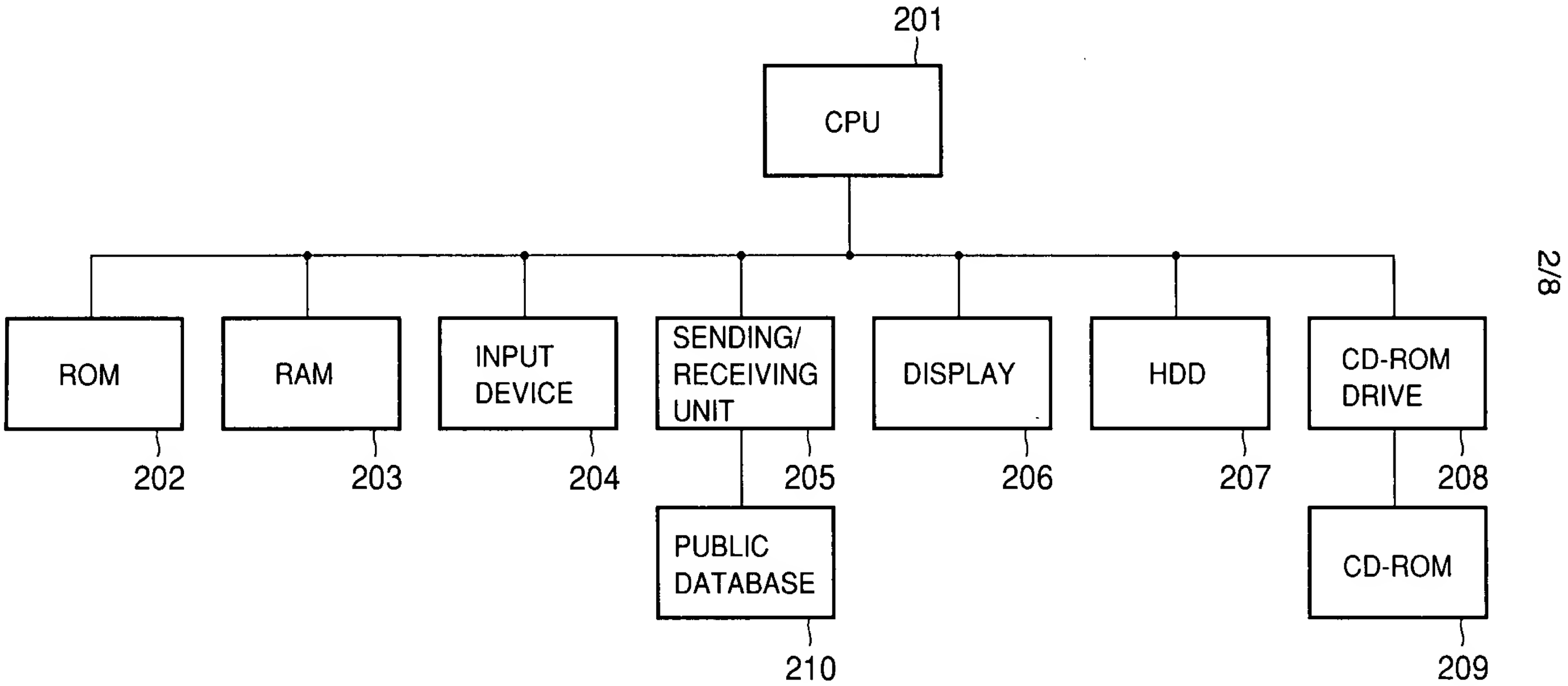

201
CPU
ROM
202
RAM
203
INPUT DEVICE
204
SENDING/ RECEIVING UNIT
205
PUBLIC DATABASE
210
DISPLAY
206
HDD
207
CD-ROM DRIVE
208
CD-ROM
209

FIG.3

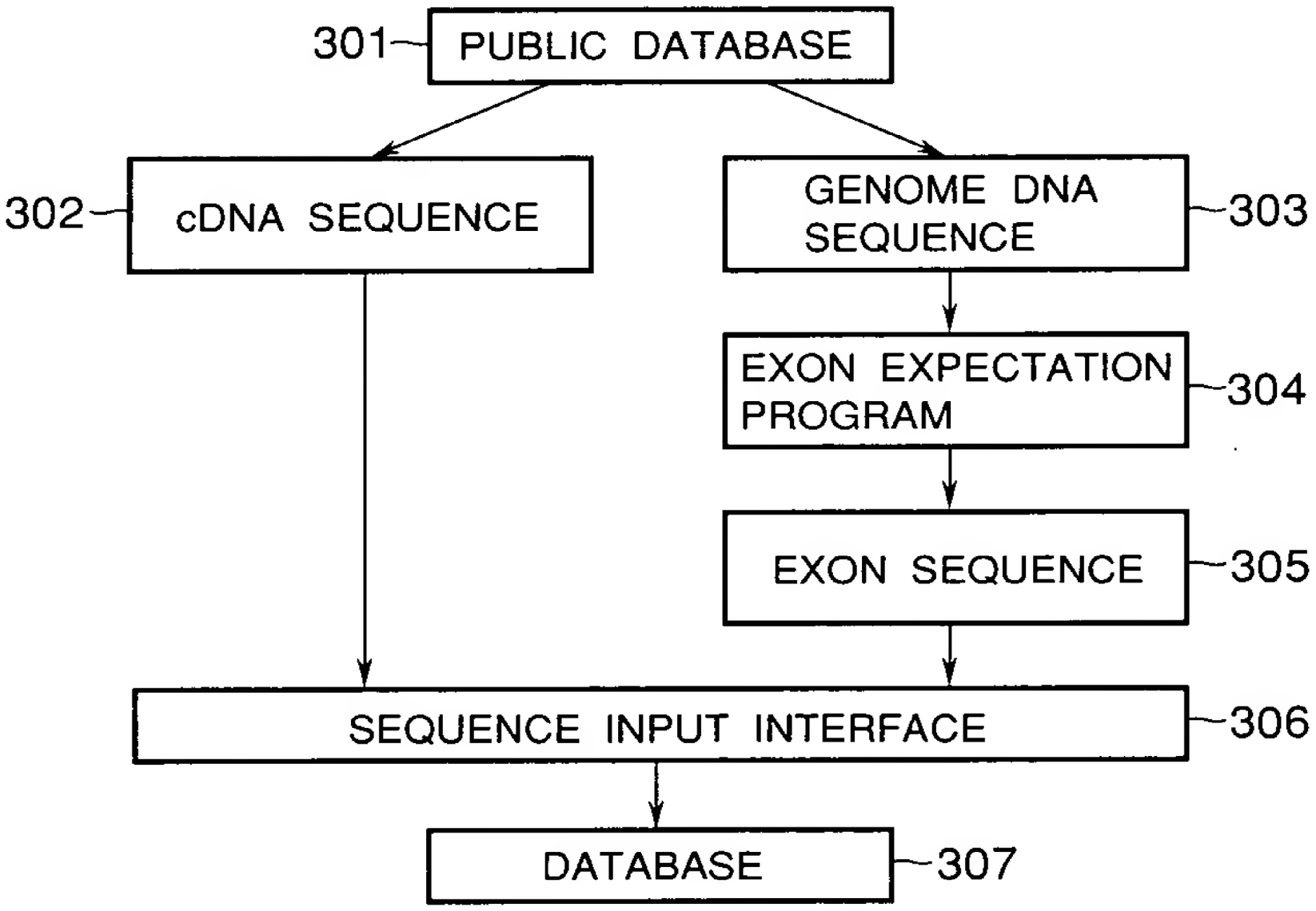

301
PUBLIC DATABASE
302
cDNA SEQUENCE
GENOME DNA SEQUENCE
303
EXON EXPECTATION PROGRAM
304
EXON SEQUENCE
305
SEQUENCE INPUT INTERFACE
306
DATABASE
307

FIG.4

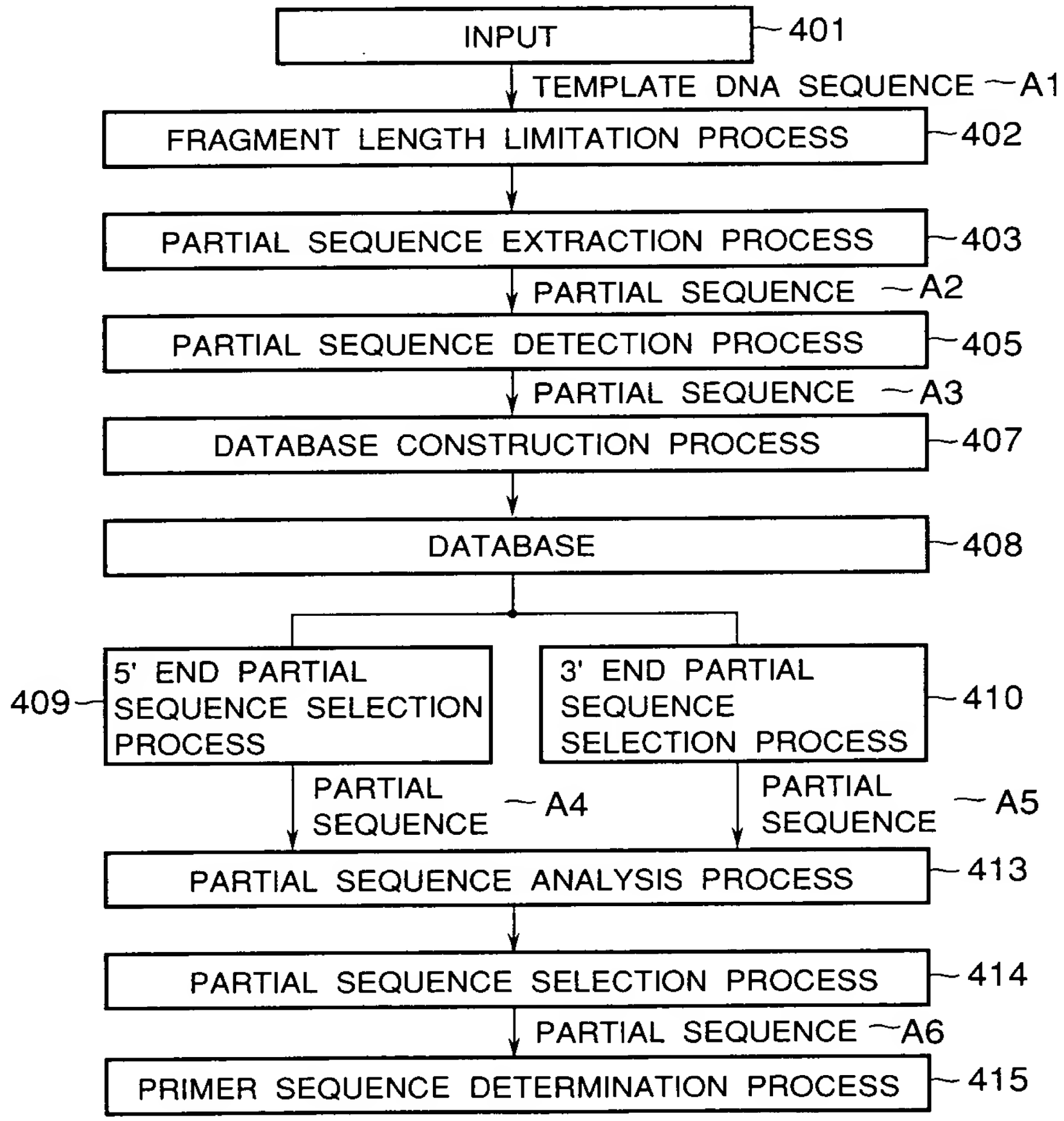

INPUT
401
TEMPLATE DNA SEQUENCE
A1
FRAGMENT LENGTH LIMITATION PROCESS
402
PARTIAL SEQUENCE EXTRACTION PROCESS
403
PARTIAL SEQUENCE
A2
PARTIAL SEQUENCE DETECTION PROCESS
405
PARTIAL SEQUENCE
A3
DATABASE CONSTRUCTION PROCESS
407
DATABASE
408
409
5' END PARTIAL SEQUENCE SELECTION PROCESS
3' END PARTIAL SEQUENCE SELECTION PROCESS
410
PARTIAL SEQUENCE
A4
PARTIAL SEQUENCE
A5
PARTIAL SEQUENCE ANALYSIS PROCESS
413
PARTIAL SEQUENCE SELECTION PROCESS
414
PARTIAL SEQUENCE
A6
PRIMER SEQUENCE DETERMINATION PROCESS
415

FIG.5

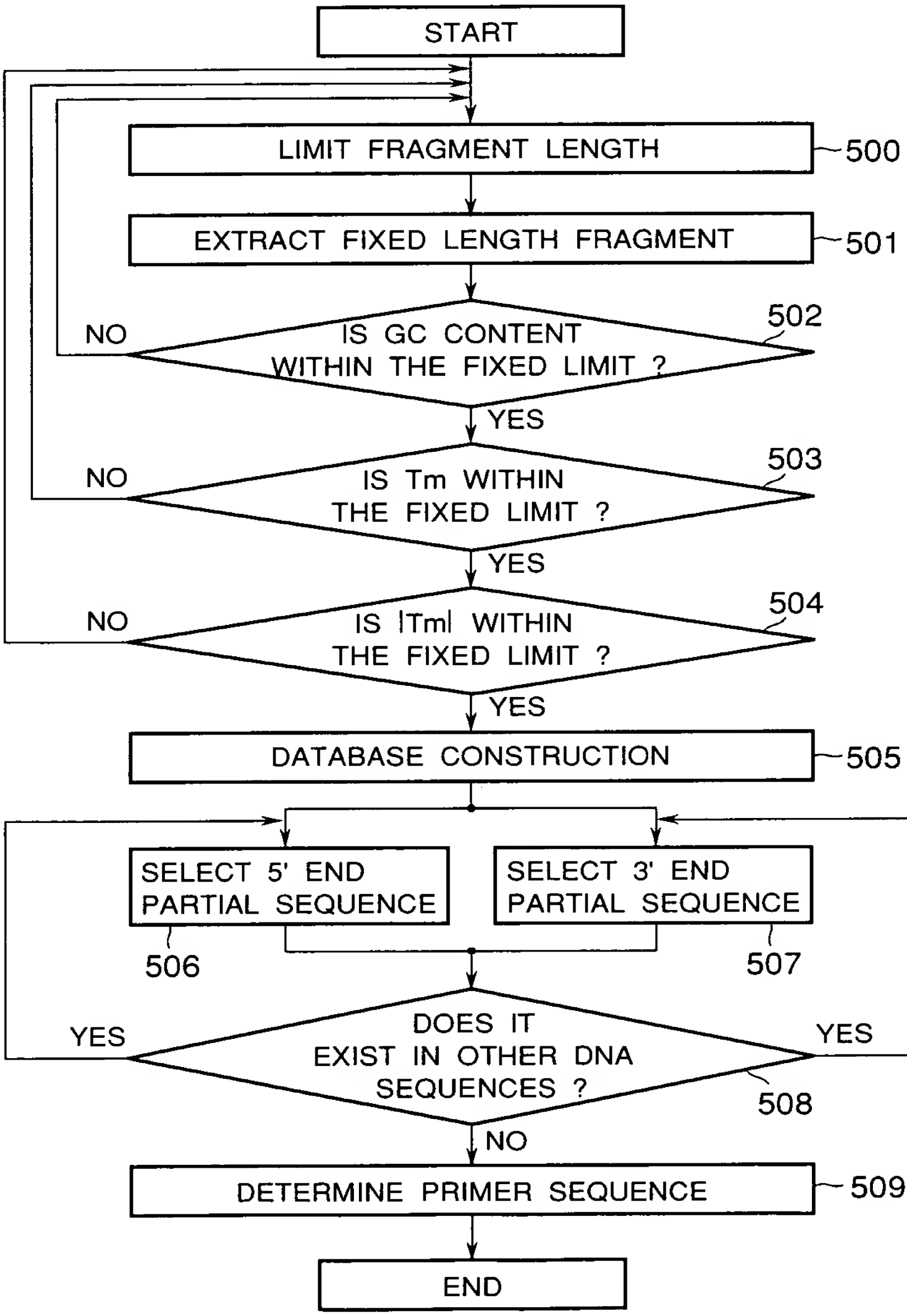

START
LIMIT FRAGMENT LENGTH
500
EXTRACT FIXED LENGTH FRAGMENT
501
IS GC CONTENT WITHIN THE FIXED LIMIT ?
502
NO
YES
IS Tm WITHIN THE FIXED LIMIT ?
503
NO
YES
IS |Tm| WITHIN THE FIXED LIMIT ?
504
NO
YES
DATABASE CONSTRUCTION
505
SELECT 5' END PARTIAL SEQUENCE
506
SELECT 3' END PARTIAL SEQUENCE
507
DOES IT EXIST IN OTHER DNA SEQUENCES ?
508
YES
YES
NO
DETERMINE PRIMER SEQUENCE
509
END

FIG.6

EXON 1

```
  1 acaacagaacaacagggagccctatcttcagaactgccaagcacatcaccttcatcagtt
 61 gctgccatttcatcgagatcagtaatacacaaaccatttactcagtcccggatacctcca
121 gatttgcccatgcatccggcaccaaggcacataacggaggaagaactttctgtgctggaa
181 agttgtttacatcgctggaggacagaaatagaaaatgacaccagagg
```

Tm	GC CONTENT	SEQUENCE
Tm=60	50.0%	acaacagaacaacagggaagc 5'
Tm=58	45.0%	aagataaagacaggaggtcg 3'

EXON 2

```
  1 acaagcagcaggagacccagaatatctagagcagccatcaagaagtgatttctcaaagca
 61 cttgaaagaagaaactattcaaataattaccaaggcatcacatgagcatgaagataaaag
121 tcctgaaacagttttgcagtcgg
```

Tm	GC CONTENT	SEQUENCE
Tm=62	55.0%	aagcagcaggagacccagaa 5'
Tm=58	45.0%	ggctgacgttttgacaaagt 3'

EXON 3

```
  1 aacctgaaaatactacaagccaaccactttctaatcagcgagttgtagaggtggcgatcc
 61 ctcatgtagggaaatttatgattgaatcaaaggaggggggtatgatgacgagg
```

Tm	GC CONTENT	SEQUENCE
Tm=58	45.0%	actacaagccaaccactttc 5'
Tm=62	55.0%	agtagtatgggggggaggaa 3'

EXON 4

```
  1 tccttaatttaaaaaggaaacaaaaacctattctttttttttcctgcattgcattaaga
 61 aattaaatgagcaagccgcagaactcttcgaatctggagaggatcgagaagtaaacaatg
121 gtttgattatcatgaatgagtttattgtcccatttttgccattattactggtggatgaaa
181 tggaagaaaaggatatactagctgtagaagatatgagaaatcgatggtgttcctaccttg
241 gtcaagaaatggaacg
```

Tm	GC CONTENT	SEQUENCE
Tm=58	45.0%	ataaatgagcaagccgcag 5'
Tm=58	45.0%	gcaaggtaaagaactggttc 3'

FIG.7

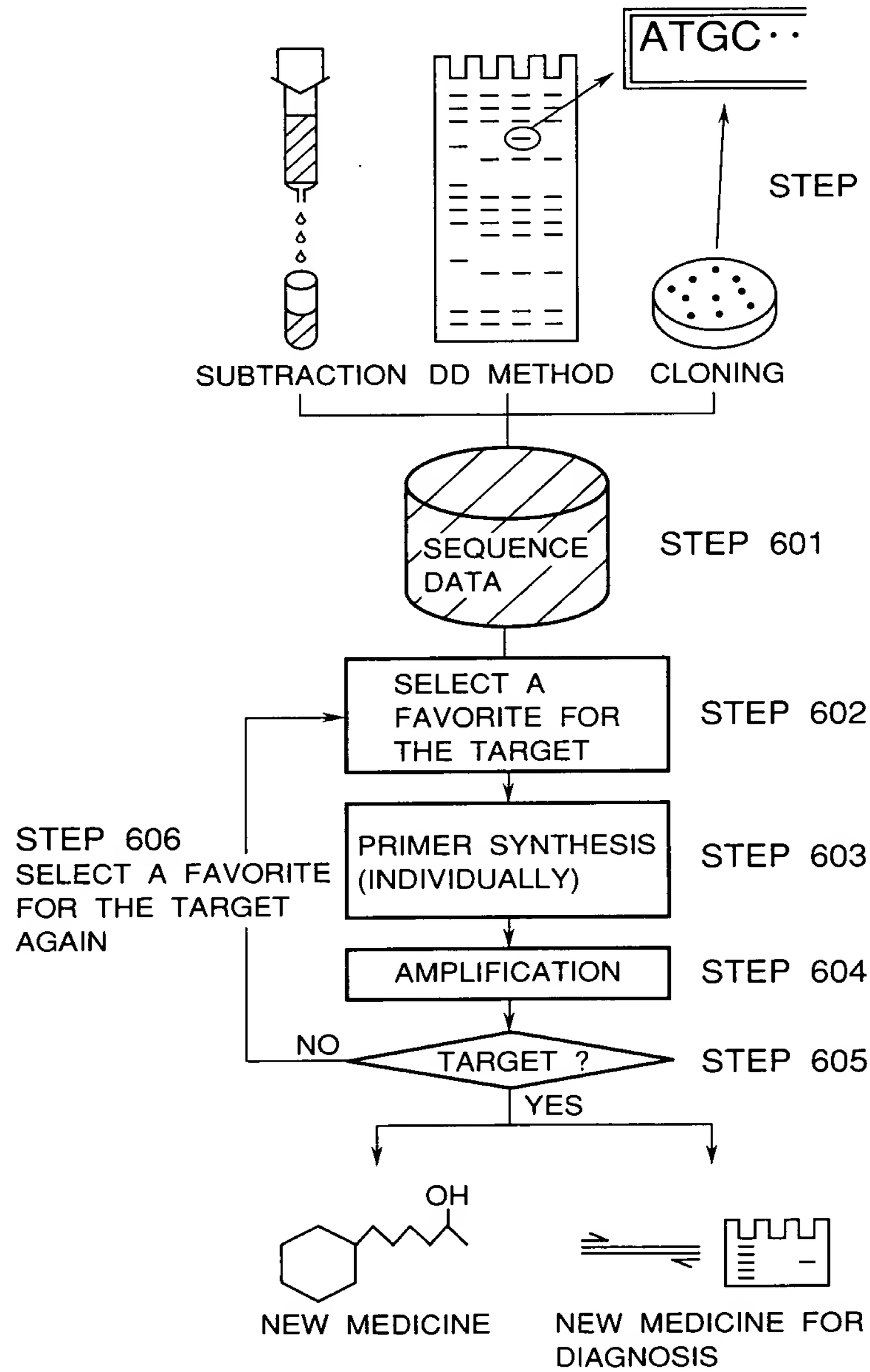
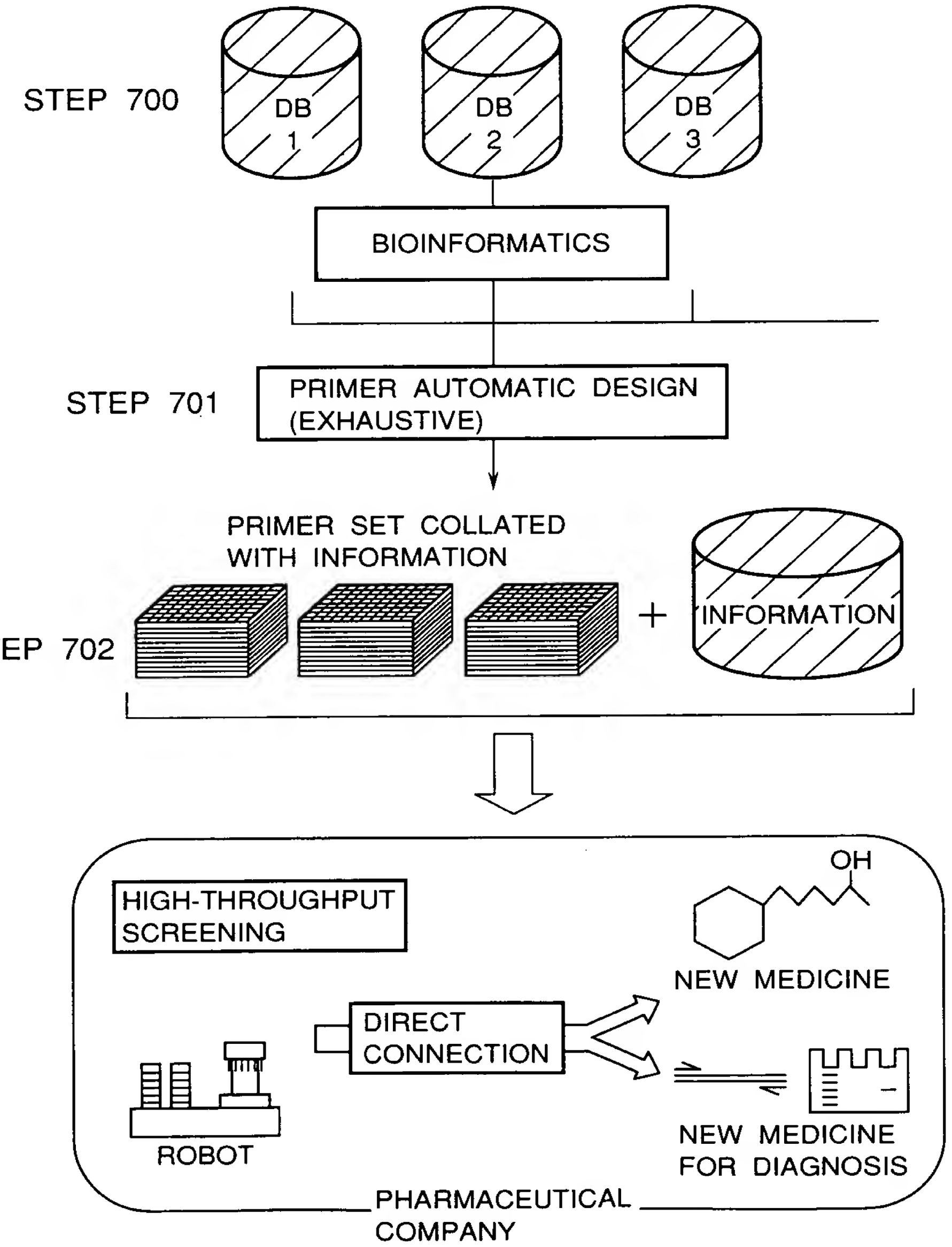

ATGC··
STEP 600
SUBTRACTION
DD METHOD
CLONING
SEQUENCE DATA
STEP 601
SELECT A FAVORITE FOR THE TARGET
STEP 602
PRIMER SYNTHESIS (INDIVIDUALLY)
STEP 603
AMPLIFICATION
STEP 604
TARGET ?
NO
STEP 605
YES
STEP 606
SELECT A FAVORITE FOR THE TARGET AGAIN
OH
NEW MEDICINE
NEW MEDICINE FOR DIAGNOSIS

FIG.8


STEP 700
DB 1
DB 2
DB 3
BIOINFORMATICS
STEP 701
PRIMER AUTOMATIC DESIGN (EXHAUSTIVE)
PRIMER SET COLLATED WITH INFORMATION
STEP 702
+
INFORMATION
HIGH-THROUGHPUT SCREENING
OH
NEW MEDICINE
DIRECT CONNECTION
ROBOT
NEW MEDICINE FOR DIAGNOSIS
PHARMACEUTICAL COMPANY